GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:49:50 ; Search time 6173 Seconds
                                          (without alignments)
                                          11028.605 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
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                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   958.4   68.2   5925   6   AR268191   AR268191 Sequence
     2   958.4   68.2   5925   6   AX009712   AX009712 Sequence

3	958.4	68.2	5925	6	AX010972	AX010972	Sequence
4	937.8	66.7	2186	6	AX744004	AX744004	Sequence
5	937.8	66.7	2790	6	AX744002	AX744002	Sequence
6	937.8	66.7	2810	6	AX744006	AX744006	Sequence
7	936.4	66.6	1440	6	AX744010	AX744010	Sequence
8	901.4	64.2	4691	6	AR370701	AR370701	Sequence
9	901.4	64.2	6166	6	AR370702	AR370702	Sequence
10	779.8	55.5	6563	6	AR116667	AR116667	Sequence
11	779.8	55.5	6563	6	CQ802871	CQ802871	Sequence
12	779.8	55.5	6563	6	AR233026	AR233026	Sequence
13	779.8	55.5	6563	6	AR237957	AR237957	Sequence
14	779.8	55.5	6563	6	BD069220	BD069220	Antibody
15	751.8	53.5	2000	6	AX774567	AX774567	Sequence
16	747.4	53.2	2178	6	AR048108	AR048108	Sequence
17	747.4	53.2	2178	6	AR054190	AR054190	Sequence
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19	747.4	53.2	2178	6	BD145002	BD145002	Human gro
20	739.6	52.6	1951	6	AX661181	AX661181	Sequence
21	739.6	52.6	6072	6	AX815239	AX815239	Sequence
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23	738.6	52.6	2143	6	AR123435	AR123435	Sequence
24	738.6	52.6	2143	6	BD132751	BD132751	Antibody
25	738.6	52.6	2143	6	AR261841	AR261841	Sequence
26	738.6	52.6	2143	6	AR491893	AR491893	Sequence
27	738.6	52.6	2143	6	BD062169	BD062169	Protein r
28	738.6	52.6	6550	6	AR126813	AR126813	Sequence
29	738.6	52.6	6550	6	AR162111	AR162111	Sequence
30	738.6	52.6	6550	6	BD224164	BD224164	Method of
31	738.6	52.6	6550	6	AX832563	AX832563	Sequence
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38	734.6	52.3	6127	6	AR454349	AR454349	Sequence
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40	689.4	49.1	2239	6	CQ877236	CQ877236	Sequence
41	689.4	49.1	2383	6	CQ877237	CQ877237	Sequence
42	638.2	45.4	784	9	AB064058	AB064058	Homo sapi
43	633.4	45.1	794	9	AB064136	AB064136	Homo sapi
44	632.2	45.0	3169	6	A57359	A57359 Sequence 5
45	632.2	45.0	3169	6	AR096536	AR096536	Sequence

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds
                                           (without alignments)
                                           10217.735 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
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Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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       Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

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3	1003	71.4	1514	12	ADG64751	Adg64751 Humanised
4	985.8	70.2	1424	13	ADR16815	Adr16815 Human bre
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6	958.4	68.2	5925	3	AAZ38770	Aaz38770 HCAT1 clo
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8	937.8	66.7	2790	10	ADD26467	Add26467 Phagemid
9	937.8	66.7	2810	10	ADD26471	Add26471 Phagemid
10	936.4	66.6	1440	10	ADD26475	Add26475 Phagemid

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13	906.2	64.5	1680	12	ADF83552	Adf83552 Anti-tete
14	901.4	64.2	4691	2	AAQ92546	Aaq92546 pComb3 ex
15	901.4	64.2	6166	2	AAQ92547	Aaq92547 Expressio
16	884.8	63.0	10251	10	ABZ37478	Abz37478 CJRA05 nu
17	856	60.9	1526	12	ADN97514	Adn97514 Artificia
18	851.8	60.6	1551	12	ADN97496	Adn97496 Artificia
19	834.8	59.4	1566	12	ADN97494	Adn97494 Artificia
20	834	59.4	2154	12	ADN97490	Adn97490 Artificia
21	820.8	58.4	1572	12	ADN97492	Adn97492 Artificia
22	820	58.4	2160	12	ADN97488	Adn97488 Artificia
23	796.8	56.7	5679	13	ADP79576	Adp79576 Plasmid p
24	779.8	55.5	6563	2	AAV44953	Aav44953 Anti-IL-8
25	779.8	55.5	6563	2	AAX90579	Aax90579 p6G4V11N3
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27	779.8	55.5	6563	3	AAC65509	Aac65509 Anti-IL-8
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35	739.6	52.6	6072	2	AAV63493	Aav63493 Fab-displ
36	739.6	52.6	6072	6	ABN85200	Abn85200 Phage-dis
37	738.6	52.6	2143	2	AAX03840	Aax03840 Plasmid p
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44	733.2	52.2	1951	6	ABQ73919	Abq73919 Plasmid p
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ALIGNMENTS

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AC    ADR16814;
XX
DT    21-OCT-2004   (first entry)
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DE    Human breast cancer-specific antibody Fab fragment DNA, Fab14.6.19.
XX
KW    Breast cancer; diagnosis; therapy; human; Fab 14.6.19; gene; ds.
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OS    Homo sapiens.
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Page 2

us-10-698-041-1.rng

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PD   05-AUG-2004.
XX
PF   30-OCT-2003; 2003US-00698041.
XX
PR   31-OCT-2002; 2002US-0423052P.
XX
PA   (CORO/) CORONELLA-WOOD J.
XX
PI   Coronella-Wood J;
XX
DR   WPI; 2004-570704/55.
DR   P-PSDB; ADR16816, ADR16817.
XX
PT   New isolated polynucleotides encoding breast cancer-specific antibody Fab
PT   fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing
PT   or treating breast cancer.
XX
PS   Claim 1; SEQ ID NO 1; 36pp; English.
XX
CC   The invention provides a breast cancer-specific antibody fragment
CC   polynucleotide and its corresponding polypeptide. The invention is useful
CC   as clinical reagents for the diagnosis and therapy of breast cancer. The
CC   present sequence is human breast cancer-specific antibody Fab fragment
CC   DNA, Fab14.6.19.
XX
SQ   Sequence 1405 BP; 326 A; 405 C; 381 G; 293 T; 0 U; 0 other;
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   Matches 1405;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCCAGGCGGCCGAGCTCGTGATGACTCAGTC 60
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Qy       61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120
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Db       61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120

Qy      121 GAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180
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Db      121 GAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180

Qy      181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240

Qy      241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300
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Qy      301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360
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Qy    421 TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG 480
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Qy    481 AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG 540
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Qy    601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660
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Db    601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660

Qy    661 CTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720

Qy    721 GGAATTTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGAATTTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780

Qy    781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG 840

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Qy   1021 CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA 1080
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Qy    1381 CCAGACCTACATCTGCAACGTGAAT 1405
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Db    1381 CCAGACCTACATCTGCAACGTGAAT 1405
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 10:58:17 ; Search time 877 Seconds
                                            (without alignments)
                                            9719.189 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB ID   Description
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3	985.8	70.2	1424	18	US-10-698-041-2	Sequence 2, Appli
4	958.4	68.2	5925	16	US-10-235-175-78	Sequence 78, Appl
5	923	65.7	1539	18	US-10-492-729-4	Sequence 4, Appli
6	916.6	65.2	1539	18	US-10-492-729-12	Sequence 12, Appl
7	884.8	63.0	10251	17	US-10-045-674-582	Sequence 582, App
8	856	60.9	1526	18	US-10-679-620-87	Sequence 87, Appl
9	851.8	60.6	1551	18	US-10-679-620-69	Sequence 69, Appl
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11	834	59.4	2154	18	US-10-679-620-63	Sequence 63, Appl
12	820.8	58.4	1572	18	US-10-679-620-65	Sequence 65, Appl
13	820	58.4	2160	18	US-10-679-620-61	Sequence 61, Appl
14	779.8	55.5	6563	10	US-09-726-258-61	Sequence 61, Appl
15	739.6	52.6	1951	13	US-10-011-125-1	Sequence 1, Appli
16	739.6	52.6	6072	9	US-09-056-160B-99	Sequence 99, Appl
17	739.6	52.6	6072	16	US-10-234-671-99	Sequence 99, Appl
18	738.6	52.6	2143	9	US-09-940-166A-5	Sequence 5, Appli
19	738.6	52.6	2143	18	US-10-762-967-5	Sequence 5, Appli
20	734.6	52.3	6127	9	US-09-920-171-1	Sequence 1, Appli
21	734.6	52.3	6127	15	US-10-113-996-1	Sequence 1, Appli
22	734.6	52.3	6127	18	US-10-791-619-1	Sequence 1, Appli
23	732.8	52.2	1477	19	US-10-728-420B-116	Sequence 116, App
C 24	732.8	52.2	1477	19	US-10-728-420B-117	Sequence 117, App
25	681.6	48.5	1730	14	US-10-194-975-108	Sequence 108, App
26	628	44.7	720	17	US-10-292-088-15	Sequence 15, Appl
27	627.8	44.7	720	17	US-10-292-088-63	Sequence 63, Appl
28	624.8	44.5	720	17	US-10-292-088-7	Sequence 7, Appli
29	624.8	44.5	720	17	US-10-292-088-101	Sequence 101, App
30	624.4	44.4	720	17	US-10-292-088-55	Sequence 55, Appl
31	623.2	44.4	720	17	US-10-292-088-79	Sequence 79, Appl
32	621.6	44.2	720	17	US-10-292-088-39	Sequence 39, Appl
33	620	44.1	720	17	US-10-292-088-31	Sequence 31, Appl
34	618.8	44.0	4793	18	US-10-737-290-141	Sequence 141, App
35	612.6	43.6	1081	17	US-10-466-164-33	Sequence 33, Appl
36	612.2	43.6	657	10	US-09-972-656-103	Sequence 103, App
37	609.8	43.4	649	19	US-10-714-079C-8	Sequence 8, Appli
38	606.2	43.1	944	17	US-10-108-260A-1585	Sequence 1585, Ap
39	604.6	43.0	968	10	US-09-992-600A-7	Sequence 7, Appli
40	604.6	43.0	968	10	US-09-924-340-7	Sequence 7, Appli
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42	604.6	43.0	968	10	US-09-999-570-7	Sequence 7, Appli
43	604.6	43.0	968	14	US-10-000-489-7	Sequence 7, Appli
44	604.6	43.0	968	14	US-10-000-986-7	Sequence 7, Appli
45	604.6	43.0	968	16	US-10-154-678-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-698-041-1
; Sequence 1, Application US/10698041
; Publication No. US20040151724A1
; GENERAL INFORMATION:
; APPLICANT: Coronella-Wood, Julia
; TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer
; FILE REFERENCE: 5051.057
; CURRENT APPLICATION NUMBER: US/10/698,041
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,052
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2

us-10-698-041-1.rnpb

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; SEQ ID NO 1
;    LENGTH: 1405
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-698-041-1

    Query Match            100.0%;  Score 1405;  DB 18;  Length 1405;
    Best Local Similarity  100.0%;  Pred. No. 0;
    Matches 1405;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCCAGGCGGCCGAGCTCGTGATGACTCAGTC 60
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Qy         61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120
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Db         61 TCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120

Qy        121 GAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180
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Qy        181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240
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Qy        241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300
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Qy        301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360
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Db        301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360

Qy        361 ACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420
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Db        361 ACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420

Qy        421 TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG 480
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Qy        661 CTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720
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Qy        781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG 840
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Page 3

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Db        841 GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCA 900

Qy        901 CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG 960
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Db        901 CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG 960

Qy        961 GAGTATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGC 1020
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Qy       1021 CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA 1080
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Qy       1081 CTGTACACGAGATATTGGGGGTCGTGATGCTCACTGGGGCCAGGGAACCCTGGTCACCGT 1140
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Qy       1141 CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCAC 1200
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RESULT 2
US-10-251-215-38
; Sequence 38, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Frederickson, Shana
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13

; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Assembled Degenerate Oligonucleotides
US-10-251-215-38

Query Match   71.4%; Score 1003; DB 17; Length 1514;
Best Local Similarity 83.7%; Pred. No. 7e-281;
Matches 1163; Conservative 25; Mismatches 165; Indels 36; Gaps 4;

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Db        15 GGGCCCGAGATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 74

Qy        95 GCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTG 154
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Db       120 GCCTGGTATCAGCAGAAACCAGGGAAASYTCCTAAGCTCCTGATCTATGATGCATCCGAT 179

Qy       215 CGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTATACACTG 274
             | ||| || |||||||||     |||||||:|||||||||||| || ||||||: || ||
Db       180 CTGGCATCTGGGGTCCCATCTCGGTTCARTGGCAGTGGATCTGGGACAGATTWCACTCTC 239

Qy       275 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAG-------- 326
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Qy       327 -GTCTACAAACTCCTAGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTG 385
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Qy       626 GTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAAC 685
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Db       660 AGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACCTATTG 719

Qy       746 CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCCAGGTGCAG 805
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Db     720 CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGAGGTGCAG 779

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Qy     926 GGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGTATCACAAACGACGCGGACTCC 985
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Db     900 GGGCTGGAGTGGRTCKSATTCATTAAT---ACTGGTAGTAGCGCATACTACGCGAGCTGG 956

Qy     986 GTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGGAAATG 1045
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Db     957 GCGGAAAGCCGATYCACCATCTCCAGAGACAMCGCCAAGAACTCASTGTATCTGCAAATG 1016

Qy    1046 AACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGGGTCGT 1105
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Qy    1157 AAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG 1216
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Db    1197 GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA 1256

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 07:45:31 ; Search time 4941 Seconds
                                           (without alignments)
                                           10823.780 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
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                 5: gb_est4:*
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                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
Result No.	Score	Query Match	Length	DB	ID	Description
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2	608	43.3	859	4	BG758795	BG758795 602713155
3	603.8	43.0	785	6	CB958366	CB958366 AGENCOURT
4	600.4	42.7	796	6	CB956719	CB956719 AGENCOURT
5	597.8	42.5	734	6	CB957433	CB957433 AGENCOURT
6	596.6	42.5	908	4	BG685179	BG685179 602637065
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13   574.8   40.9   765   6   CB957191        CB957191 AGENCOURT
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16   569.8   40.6   912   4   BF974515        BF974515 602243421
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18   565.4   40.2   766   6   CB956983        CB956983 AGENCOURT
19   564.2   40.2   710   4   BI908471        BI908471 603069231
20   563.8   40.1   774   4   BM007808        BM007808 603617276
21   562.2   40.0   875   4   BI518518        BI518518 603061638
22   560.2   39.9   898   5   BQ708918        BQ708918 AGENCOURT
23   558.2   39.7   816   4   BI759427        BI759427 603043095
24   556     39.6   931   4   BG757255        BG757255 602715238
25   556     39.6   962   4   BI819546        BI819546 603036758
26   552.6   39.3   934   4   BF974268        BF974268 602243920
27   552.4   39.3   817   6   CB957285        CB957285 AGENCOURT
28   550     39.1   770   4   BG530186        BG530186 602558684
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34   539.2   38.4   918   4   BG681688        BG681688 602627806
c 35 537.2   38.2   615   2   AW603541        AW603541 RC0-CN002
36   536.4   38.2   795   6   CB958667        CB958667 AGENCOURT
37   535.8   38.1   849   7   CO578998        CO578998 ILLUMIGEN
38   533     37.9   706   6   CB956177        CB956177 AGENCOURT
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40   532.4   37.9   726   4   BM007723        BM007723 603617168
41   532.4   37.9   731   6   CB955606        CB955606 AGENCOURT
42   531.4   37.8   697   6   CD684481        CD684481 EST1001 h
43   531     37.8   971   7   CO580847        CO580847 ILLUMIGEN
44   530     37.7   907   5   BQ708655        BQ708655 AGENCOURT
45   529.4   37.7   700   4   BG547577        BG547577 602575404
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ALIGNMENTS

RESULT 1
BQ712430
LOCUS   BQ712430   995 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
            5', mRNA sequence.
ACCESSION   BQ712430
VERSION   BQ712430.1 GI:21851329
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 995)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

FEATURES   Location/Qualifiers
     source   1. .995
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277729"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

   Query Match   43.8%; Score 615.4; DB 5; Length 995;
   Best Local Similarity   96.7%; Pred. No. 2.2e-160;
   Matches 639; Conservative   0; Mismatches   21; Indels   1; Gaps   1;

Qy   41 GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 100
             || | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   67 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 126

Qy   101 ATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGG 160
             |||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||
Db   127 ATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTAGATTGG 186

Qy   161 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCC 220
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   187 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCC 246

Qy   221 TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATC 280
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   247 TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 306

Qy   281 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCT 340
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   307 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCCG 366

Qy   341 AGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTC 400
             || || ||||| ||||| ||||||||| ||||||||||||||||||||||||||
Db   367 TACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC 426

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Qy   401 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   427 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 486

Qy   461 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   487 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 546

Qy   521 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   547 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 606

Qy   581 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   607 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 666

Qy   641 GTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTC-AACAGGGGAGAGTGTTA 699
         |||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||
Db   667 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCNAACAGGGGAGAGTGTTA 726

Qy   700 G 700
         |
Db   727 G 727
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 12:20:41 ; Search time 121 Seconds
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Title: US-10-698-041-1
Perfect score: 2494
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Scoring table: BLOSUM62
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                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155500_6534/app_query.fasta_1.15
43
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Database :   A_Geneseq_16Dec04:*
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                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1802	72.3	628	6	ABJ38670	Abj38670 Fab expre
2	1802	72.3	638	6	ADA89103	Ada89103 Phage dis
3	1802	72.3	638	6	ADA90139	Ada90139 Anti-Abet
4	1802	72.3	638	6	ADA91410	Ada91410 Anti-Abet
5	1802	72.3	747	7	ADG74355	Adg74355 MSPRO lig
6	1768.5	70.9	490	3	AAY56637	Aay56637 hCAT1 bin
7	1733	69.5	484	6	ABR55341	Abr55341 Amino aci
8	1676	67.2	537	3	AAB03664	Aab03664 Anti-CD18
9	1675	67.2	698	2	AAW83493	Aaw83493 4D5 Fab m
10	1668.5	66.9	650	5	ABP61241	Abp61241 Phage-dis
11	1665.5	66.8	502	8	ADN97515	Adn97515 Artificia
12	1664.5	66.7	512	8	ADN97497	Adn97497 Artificia
13	1660	66.6	517	8	ADN97495	Adn97495 Artificia
14	1658	66.5	519	8	ADN97493	Adn97493 Artificia
15	1650	66.2	713	8	ADN97491	Adn97491 Artificia
16	1648	66.1	715	8	ADN97489	Adn97489 Artificia
17	1606.5	64.4	487	6	ABO27163	Abo27163 Humanised
18	1282.5	51.4	712	8	ADN97543	Adn97543 Artificia
19	1213.5	48.7	1031	5	ADI46109	Adi46109 Single st
20	1178	47.2	483	8	ADN97549	Adn97549 Artificia
21	1178	47.2	510	8	ADN97519	Adn97519 Artificia
22	1178	47.2	510	8	ADN97501	Adn97501 Artificia
23	1178	47.2	700	8	ADN97521	Adn97521 Artificia
24	1142	45.8	219	8	ADR16817	Adr16817 Human bre
25	1115.5	44.7	500	7	ADD13792	Add13792 Plasmid p
26	1104	44.3	523	3	AAY44994	Aay44994 HD70scFv-
27	1098	44.0	239	7	ADE28405	Ade28405 Human ant
28	1097	44.0	238	8	ADL93650	Adl93650 Human CD4
29	1097	44.0	239	7	ADE28465	Ade28465 Human ant
30	1095	43.9	238	8	ADL93653	Adl93653 Human CD4
31	1094	43.9	238	8	ADL93654	Adl93654 Human CD4
32	1093	43.8	239	7	ADE28421	Ade28421 Human ant
33	1093	43.8	239	7	ADE28521	Ade28521 Human ant
34	1092	43.8	239	7	ADE28397	Ade28397 Human ant
35	1090	43.7	239	7	ADE28469	Ade28469 Human ant
36	1090	43.7	239	7	ADE28477	Ade28477 Human ant
37	1088	43.6	219	7	ADJ32150	Adj32150 Human int
38	1088	43.6	238	8	ADL93649	Adl93649 Human CD4
39	1082	43.4	238	8	ADL93652	Adl93652 Human CD4
40	1079	43.3	239	7	ADE28461	Ade28461 Human ant
41	1077.5	43.2	237	8	ADL93657	Adl93657 Human CD4
42	1077	43.2	239	3	AAY82615	Aay82615 Human PTH
43	1075.5	43.1	237	8	ADL93658	Adl93658 Human CD4
44	1075.5	43.1	237	8	ADL93651	Adl93651 Human CD4
45	1073	43.0	239	3	AAY82616	Aay82616 Human PTH

ALIGNMENTS

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ID   ABJ38670 standard; protein; 628 AA.
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AC   ABJ38670;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Fab expression vector protein SEQ ID No 96.
XX
KW   Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;
KW   antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;
KW   constitutive activation; craniosynostosis; cell proliferative disorder;
KW   achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;
KW   hypochondroplasia; severe achondroplasia; transitional cell carcinoma;
KW   Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;
KW   tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;
KW   mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;
KW   Fab.
XX
OS   Homo sapiens.
XX
PN   WO2002102854-A2.
XX
PD   27-DEC-2002.
XX
PF   20-JUN-2002; 2002WO-IB003523.
XX
PR   20-JUN-2001; 2001US-0299187P.
XX
PA   (MORP-) MORPHOSYS AG.
PA   (PROC-) PROCHON BIOTECH LTD.
XX
PI   Thomassen-Wolf E,  Borges E,  Yayon A,  Rom E;
XX
DR   WPI; 2003-167489/16.
XX
PT   New molecules having the antigen-binding portion of antibodies that block
PT   activation of receptor protein tyrosine kinase, useful for treating or
PT   inhibiting skeletal dysplasias, craniosynostosis or cell proliferative
PT   disorders.
XX
PS   Disclosure; Fig 26B; 103pp; English.
XX
CC   The invention relates to a novel molecule comprising the antigen binding
CC   portion of an isolated antibody, which has an increased affinity for a
CC   receptor protein tyrosine kinase and which blocks constitutive activation
CC   of the receptor protein tyrosine kinase. The methods and compositions of
CC   the invention are useful for treating or inhibiting a skeletal dysplasia,
CC   craniosynostosis or a cell proliferative disorder. The skeletal dysplasia
CC   is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe
CC   achondroplasia with developmental delay or acanthosis nigricans
CC   dysplasia. The craniosynostosis disorder is Muenke coronal
CC   craniosynostosis or Crouzin syndrome with acanthosis nigricans. The cell
CC   proliferative disorder is tumour progression that is progression of
CC   transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple
CC   myeloma or mammary carcinoma. This sequence represents the protein
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Alignment Scores:
Pred. No.:             1.3e-132      Length:         628
Score:                 1802.00       Matches:        370
Percent Similarity:    83.47%        Conservative:   24
Best Local Similarity: 78.39%        Mismatches:     52
Query Match:           72.25%        Indels:         26
DB:                    6             Gaps:           7
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US-10-698-041-1 (1-1405) x ABJ38670 (1-628)

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Qy        8 CTGGCTGGTTTCGCTACCGTGGCCCAGGCGGCCGAGCTCGTGATGACTCAGTCTCCACTC 67
            |||||||||||||||||||||||||||||||    |||::::::|||:::|||||||||||
Db        2 LeuAlaGlyPheAlaThrValAlaGln---AlaAspIleValLeuThrGlnSerProAla 20

Qy       68 TCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTC 127
            :::|||    ::::::|||||||||    |||::::::|||||||||:::|||||||||:::
Db       21 ThrLeuSerLeuSerProGlyGluArgAlaThrLeuSerCysArgAlaSerGlnSerVal 40

Qy      128 CTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA 187
               |||         ||||||   ||||||   |||||||||||||||:::|||
Db       41 SerSerSer-----------TyrLeuAlaTrpTyrGlnGlnLysProGlyGlnAlaPro 56

Qy      188 CAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGC 247
            :::|||||||||||||         :::|||||||:::|||||||||    |||||||||||
Db       57 ArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyValProAlaArgPheSerGly 76

Qy      248 AGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGG 307
            |||||||||||||||||||||:::|||||||   ||||||   :::|||   |||||||
Db       77 SerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGluProGluAspPheAla 96

Qy      308 GTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGACACGACTG 367
            |||||||||||||   |||      ||||||   ||||||||||||||||||||:::::::
Db       97 ValTyrTyrCysGlnGlnHisTyrThrThrProProThrPheGlyGlnGlyThrLysVal 116

Qy      368 GAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAG 427
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      117 GluIleLysArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGln 136

Qy      428 TTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC 487
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      137 LeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAla 156

Qy      488 AAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA 547
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      157 LysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThr 176

Qy      548 GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCA 607
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      177 GluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAla 196

Qy      608 GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCC 667
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
```

```
Db      197  AspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerPro 216

Qy      668  GTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTT 727
             |||||||||||||||||||||||||||||
Db      217  ValThrLysSerPheAsnArgGlyGluAla----------------------------- 226

Qy      728  AAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCA 787
              ||||||          |||    |||          ||||||    |||          |||
Db      227  ---MetLysGln------SerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrPro 243

Qy      788  ---GCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGGGGGG 844
                |||||||||||||||    |||||||||||||||||||||||||||||||||||||
Db      244  ValThrLysAlaGlnValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGly 263

Qy      845  TCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGG 904
             |||||||||||||||||    |||||||||:::|||||||||:::|||    |||    |||
Db      264  SerLeuArgLeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrp 283

Qy      905  GTCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGT 964
             |||||||||    |||||||||||||||    |||||||||    |||:::          |||
Db      284  ValArgGlnAlaProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGly 303

Qy      965  ATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAG 1024
              |||          |||||||||||||||||||||||    |||||||||||||||||||||:::|||
Db      304  SerThrTyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLys 323

Qy      1025 AACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGT 1084
             ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db      324  AsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCys 343

Qy      1085 ACACGAGATATTGGGGGTCGTGATGCT---------------CACTGGGGCCAGGGAACC 1129
              |||          |||    |||                          :::|||||||||||||||
Db      344  AlaArg------TrpGlyGlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThr 361

Qy      1130 CTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      362  LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 381

Qy      1190 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382  SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 401

Qy      1250 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      402  GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 421

Qy      1310 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      422  AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer 441

Qy      1370 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT 1405
             ||||||||||||||||||||||||||||||||||||
Db      442  SerLeuGlyThrGlnThrTyrIleCysAsnValAsn 453
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 14:34:27 ; Search time 165 Seconds
                                            (without alignments)
                                            5660.373 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 2843670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-MAXLEN=2000000000 -USER=US10698041_@CGN_1_1_128_@runat_14042005_155503_6665
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                  9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                  10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                  11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                  12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                  13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                  14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                  15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                  16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                  17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                  18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

            19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
            20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1699.5	68.1	4852	15	US-10-412-406-33	Sequence 33, Appl
2	1697.5	68.1	663	15	US-10-412-406-32	Sequence 32, Appl
3	1668.5	66.9	491	13	US-10-011-125-2	Sequence 2, Appli
4	1665.5	66.8	502	16	US-10-679-620-88	Sequence 88, Appl
5	1664.5	66.7	512	16	US-10-679-620-70	Sequence 70, Appl
6	1660	66.6	517	16	US-10-679-620-68	Sequence 68, Appl
7	1658	66.5	519	16	US-10-679-620-66	Sequence 66, Appl
8	1650	66.2	713	16	US-10-679-620-64	Sequence 64, Appl
9	1648	66.1	715	16	US-10-679-620-62	Sequence 62, Appl
10	1282.5	51.4	712	16	US-10-679-620-116	Sequence 116, App
11	1178	47.2	483	16	US-10-679-620-122	Sequence 122, App
12	1178	47.2	510	16	US-10-679-620-74	Sequence 74, Appl
13	1178	47.2	510	16	US-10-679-620-92	Sequence 92, Appl
14	1178	47.2	700	16	US-10-679-620-94	Sequence 94, Appl
15	1142	45.8	219	16	US-10-698-041-4	Sequence 4, Appli
16	1098	44.0	239	15	US-10-292-088-16	Sequence 16, Appl
17	1097	44.0	238	16	US-10-663-244-145	Sequence 145, App
18	1097	44.0	239	15	US-10-292-088-56	Sequence 56, Appl
19	1095	43.9	238	16	US-10-663-244-148	Sequence 148, App
20	1094	43.9	238	16	US-10-663-244-149	Sequence 149, App
21	1093	43.8	239	15	US-10-292-088-32	Sequence 32, Appl
22	1093	43.8	239	15	US-10-292-088-102	Sequence 102, App
23	1092	43.8	239	15	US-10-292-088-8	Sequence 8, Appli
24	1090	43.7	239	15	US-10-292-088-64	Sequence 64, Appl
25	1090	43.7	239	15	US-10-292-088-80	Sequence 80, Appl
26	1088	43.6	219	10	US-09-972-656-104	Sequence 104, App
27	1088	43.6	238	16	US-10-663-244-144	Sequence 144, App
28	1082	43.4	238	16	US-10-663-244-147	Sequence 147, App
29	1079	43.3	239	15	US-10-292-088-40	Sequence 40, Appl
30	1077.5	43.2	237	16	US-10-663-244-152	Sequence 152, App
31	1075.5	43.1	237	16	US-10-663-244-146	Sequence 146, App
32	1075.5	43.1	237	16	US-10-663-244-153	Sequence 153, App
33	1067	42.8	239	15	US-10-108-260A-4028	Sequence 4028, Ap
34	1060	42.5	239	10	US-09-992-600A-8	Sequence 8, Appli
35	1060	42.5	239	10	US-09-924-340-8	Sequence 8, Appli
36	1060	42.5	239	10	US-09-992-095B-8	Sequence 8, Appli
37	1060	42.5	239	10	US-09-999-570-8	Sequence 8, Appli
38	1060	42.5	239	14	US-10-000-489-8	Sequence 8, Appli
39	1060	42.5	239	14	US-10-000-986-8	Sequence 8, Appli
40	1060	42.5	239	14	US-10-154-678-8	Sequence 8, Appli
41	1060	42.5	239	17	US-10-838-854-8	Sequence 8, Appli
42	1052.5	42.2	220	9	US-09-822-698A-24	Sequence 24, Appl
43	1048	42.0	247	15	US-10-466-164-69	Sequence 69, Appl
44	1047	42.0	219	10	US-09-972-656-106	Sequence 106, App
45	1044	41.9	239	15	US-10-404-724-12	Sequence 12, Appl

RESULT 15
US-10-698-041-4
; Sequence 4, Application US/10698041
; Publication No. US20040151724A1

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;  GENERAL INFORMATION:
;    APPLICANT: Coronella-Wood, Julia
;    TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer
;    FILE REFERENCE: 5051.057
;    CURRENT APPLICATION NUMBER: US/10/698,041
;    CURRENT FILING DATE:  2003-10-30
;    PRIOR APPLICATION NUMBER: US 60/423,052
;    PRIOR FILING DATE: 2002-10-31
;    NUMBER OF SEQ ID NOS: 6
;    SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;    LENGTH: 219
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-698-041-4
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Alignment Scores:
Pred. No.:                6.37e-69        Length:         219
Score:                    1142.00         Matches:        219
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              45.79%          Indels:         0
DB:                       16              Gaps:           0
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US-10-698-041-1 (1-1405) x US-10-698-041-4 (1-219)

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Qy        41 GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 100
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Db         1 GluLeuValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

Qy       101 ATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGG 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40

Qy       161 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCC 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlyPheAsnArgAla 60

Qy       221 TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATC 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspTyrThrLeuLysIle 80

Qy       281 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCT 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlyLeuGlnThrPro 100

Qy       341 AGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTC 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 ArgThrPheGlyGlnGlyThrArgLeuGluIleLysArgThrValAlaAlaProSerVal 120

Qy       401 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 PheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeu 140

Qy       461 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 LeuAsnAsnPheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGln 160

Qy       521 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 SerGlyAsnSerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu 180

Qy       581 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 640
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                          us-10-698-041-1.n2p.rapb
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Db        181 SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGlu 200

Qy        641 GTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ValThrHisGlnGlyLeuSerLeuProValThrLysSerPheAsnArgGlyGluCys 219
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Search completed: April 15, 2005, 14:54:48
Job time : 190 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 14:02:16 ; Search time 31.5 Seconds
                                               (without alignments)
                                               8583.146 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155501_6556/app_query.fasta_1.15
43
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041_@CGN_1_1_37_@runat_14042005_155501_6556 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
                  1: pir1:*
                  2: pir2:*
                  3: pir3:*
                  4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	897	36.0	215	2	JE0242	Ig kappa chain NIG
2	874	35.0	215	2	JE0244	Ig kappa chain NIG
3	856	34.3	215	2	JE0243	Ig kappa chain NIG
4	848.5	34.0	216	2	JE0241	Ig kappa chain Am3
5	843	33.8	215	2	A23746	Ig kappa chain V-I
6	800	32.1	219	2	S52028	Ig kappa chain - m
7	800	32.1	219	2	PC4203	Ig kappa chain (mo
8	789	31.6	219	2	S16112	Ig kappa chain V r
9	785	31.5	219	2	S38865	Ig kappa chain - m
10	778	31.2	217	2	S42772	Ig kappa chain - m
11	756	30.3	225	2	JL0029	Ig kappa chain pre
12	741.5	29.7	240	2	S06084	Ig kappa chain pre
13	728	29.2	220	2	A49444	Ig gamma-1 heavy c
14	702.5	28.2	220	2	A31790	Ig kappa chain V r
15	693.5	27.8	218	2	S68241	Ig kappa chain V r
16	680.5	27.3	218	2	JC5810	monoclonal antibod
17	677.5	27.2	214	2	S68212	Ig kappa chain (Ma
18	665	26.7	548	2	S38864	Ig epsilon chain C
19	660.5	26.5	241	2	S69131	Ig heavy chain (DO
20	655.5	26.3	210	2	A56169	Ig kappa chain V r
21	655.5	26.3	213	2	S68213	Ig heavy chain (Ma
22	655.5	26.3	234	2	S01320	Ig kappa chain pre
23	655	26.3	197	2	S29593	Ig kappa chain (WM
24	649.5	26.0	230	2	S33161	Ig kappa chain - s
25	646.5	25.9	234	2	S14237	Ig kappa chain pre
26	639.5	25.6	225	2	S37484	Ig kappa chain - m
27	633	25.4	178	2	PT0219	Ig kappa chain V-C
28	627	25.1	235	2	S25058	Ig kappa chain - m
29	626	25.1	444	2	PC4436	monoclonal antibod
30	621	24.9	220	2	S68211	Ig heavy chain (Ma
31	600.5	24.1	254	2	B31790	Ig heavy chain V r
32	598.5	24.0	246	2	S38950	Ig gamma chain - m
33	598.5	24.0	446	2	S40295	Ig gamma-2a chain
34	594	23.8	135	2	S40342	Ig kappa chain - h
35	594	23.8	135	2	S52059	JC-kappa protein -
36	593.5	23.8	469	2	S37483	Ig gamma-2a chain
37	593	23.8	121	2	S40371	Ig kappa chain - h
38	592	23.7	474	1	G2MS11	Ig gamma-2b chain
39	576	23.1	214	2	PC4202	monoclonal antibod
40	571	22.9	136	2	S40357	Ig kappa chain V-J
41	570.5	22.9	221	2	S49220	Ig gamma-1 chain -
42	565	22.7	470	2	S22080	Ig heavy chain pre
43	560	22.5	117	1	K2HUGM	Ig kappa chain pre
44	559	22.4	143	2	S23624	Ig heavy chain V r
45	557	22.3	132	2	S26882	Ig kappa chain V r

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 12:25:16 ; Search time 145.5 Seconds
                                            (without alignments)
                                            9889.639 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155501_6542/app_query.fasta_1.1543
-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041_@CGN_1_1_197_@runat_14042005_155501_6542 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1097	44.0	239	2	Q8NEK0	Q8nek0 homo sapien
2	1070.5	42.9	240	2	Q6PIH6	Q6pih6 homo sapien
3	992	39.8	239	2	Q8TCD0	Q8tcd0 homo sapien
4	992	39.8	239	2	Q6P491	Q6p491 homo sapien
5	904.5	36.3	236	2	Q6PIL8	Q6pil8 homo sapien
6	888	35.6	235	2	Q6GMV9	Q6gmv9 homo sapien

7	888	35.6	470	2	Q6PJA4	Q6pja4 homo sapien
8	878	35.2	235	2	Q6PJF2	Q6pjf2 homo sapien
9	877.5	35.2	236	2	Q6P5S8	Q6p5s8 homo sapien
10	876	35.1	478	2	Q6PI81	Q6pi81 homo sapien
11	873.5	35.0	466	2	Q6N096	Q6n096 homo sapien
12	865	34.7	235	2	Q6GMW0	Q6gmw0 homo sapien
13	864.5	34.7	472	2	Q6N089	Q6n089 homo sapien
14	852.5	34.2	236	2	Q6GMW1	Q6gmw1 homo sapien
15	852	34.2	465	2	Q6P6C4	Q6p6c4 homo sapien
16	849.5	34.1	234	2	Q7Z473	Q7z473 homo sapien
17	846.5	33.9	236	2	Q6GMX0	Q6gmx0 homo sapien
18	845	33.9	466	2	Q6IN78	Q6in78 homo sapien
19	842.5	33.8	473	2	Q6MZV7	Q6mzv7 homo sapien
20	838.5	33.6	236	2	Q6GMX8	Q6gmx8 homo sapien
21	838.5	33.6	236	2	Q7Z3Y4	Q7z3y4 homo sapien
22	836	33.5	544	2	Q6PJ95	Q6pj95 homo sapien
23	835.5	33.5	236	2	Q6PIT5	Q6pit5 homo sapien
24	835	33.5	236	2	Q6ZP85	Q6zp85 homo sapien
25	834	33.4	475	2	Q6MZQ6	Q6mzq6 homo sapien
26	833.5	33.4	236	2	Q6PIH7	Q6pih7 homo sapien
27	829.5	33.3	464	2	Q6MZU6	Q6mzu6 homo sapien
28	827	33.2	470	2	Q7Z5W1	Q7z5w1 homo sapien
29	818.5	32.8	236	2	Q6GMX9	Q6gmx9 homo sapien
30	815.5	32.7	475	2	Q6GMW7	Q6gmw7 homo sapien
31	812	32.6	473	2	Q6P055	Q6p055 homo sapien
32	808.5	32.4	236	2	Q6PIH4	Q6pih4 homo sapien
33	807	32.4	480	2	Q6N094	Q6n094 homo sapien
34	792.5	31.8	521	2	Q8N4Y9	Q8n4y9 homo sapien
35	789	31.6	219	2	Q65ZC0	Q65zc0 mus musculu
36	785.5	31.5	482	2	Q7Z351	Q7z351 homo sapien
37	772	31.0	475	2	Q6N095	Q6n095 homo sapien
38	765	30.7	481	2	Q6N097	Q6n097 homo sapien
39	761.5	30.5	465	2	Q6GMX6	Q6gmx6 homo sapien
40	759	30.4	493	2	Q68CN4	Q68cn4 homo sapien
41	741	29.7	476	2	Q6GMX1	Q6gmx1 homo sapien
42	736.5	29.5	518	2	Q6N030	Q6n030 homo sapien
43	734.5	29.5	469	2	Q7Z7P5	Q7z7p5 homo sapien
44	725	29.1	480	2	Q6PJF1	Q6pjf1 homo sapien
45	702	28.1	417	2	Q6N093	Q6n093 homo sapien

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 08:20:56 ; Search time 263 Seconds
                                           (without alignments)
                                           8741.326 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	958.4	68.2	5925	4	US-09-315-926A-78	Sequence 78, Appl
2	901.4	64.2	4691	3	US-08-591-632-43	Sequence 43, Appl
3	901.4	64.2	4691	3	US-09-611-451-43	Sequence 43, Appl
4	901.4	64.2	6166	3	US-08-591-632-51	Sequence 51, Appl
5	901.4	64.2	6166	3	US-09-611-451-51	Sequence 51, Appl
6	779.8	55.5	6563	3	US-09-027-449-61	Sequence 61, Appl
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25    734.6    52.3    6127    4    US-09-920-171-1       Sequence 1, Appli
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ALIGNMENTS

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; Sequence 78, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmuth
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
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;   LOCATION: (1)..(5925)
;   OTHER INFORMATION: /note="Nucleotide hCAT1 encoding sequence
US-09-315-926A-78

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Qy     351 GCCAAGGGACACGACTGGAGATTAAAC---GAACTGTGGCTGCACCATCTGTCTTCATCT 407
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Qy     648 ATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA-------G 700
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Page 3

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us-10-698-041-1.n2p.rai

GenCore version 5.1.6
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

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     2   1060   42.5   239 4 US-10-000-489-8   Sequence 8, Appli

Page 1

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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 491
;   TYPE: PRT

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;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2
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Query Match:	66.90%	Indels:	37
DB:	4	Gaps:	7

US-10-698-041-1 (1-1405) x US-10-011-125A-2 (1-491)

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Qy      815 TCCGGGGGGAGGCTTAGTTCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGA 874
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      267 SerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaAlaSerGly 286

Qy      875 TACACCTTCAGCAATTACTGGATGCACTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTG 934
            |||||||||:::||||||    |||:::|||:::||||||    ||||||||||||||||
Db      287 TyrThrPheThrAsnTyrGlyMetAsnTrpIleArgGlnAlaProGlyLysGlyLeuGlu 306

Qy      935 TGGGTCTCACGTATTAATGAA---GATGGGAGTATCACAAACGACGCGGACTCCGTGAAG 991
            ||||||    |||||||    |||    |||    |||    ||||||    |||    |||
Db      307 TrpValGlyTrpIleAsnThrTyrThrGlyGluProThrTyrAlaAlaAsp---PheLys 325

Qy      992 GGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGGAAATGAACAGT 1051
            |||    ||||||||||    |||    :::    |||||:::||||||:::|||||||||
Db      326 ArgArgPheThrIleSerAlaAspThrSerSerAsnThrValTyrLeuGlnMetAsnSer 345

Qy     1052 CTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGA------------------- 1090
            |||||||||||||||||||||||||||||||||||||||       :::
Db      346 LeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysTyrProHisTyrTyrGlySer 365

Qy     1091 ---------------GATATTGGGGGTCGTGATGCTCACTGGGGCCAGGGAACCCTGGTC 1135
                           |||:::                  ||||||||||||||||||||||
Db      366 SerHisTrpTyrPheAspVal------------------TrpGlyGlnGlyThrLeuVal 379

Qy     1136 ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAG 1195
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Db      380 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 399

Qy     1196 AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG 1255
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Qy     1256 GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC 1315
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Db      420 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 439

Qy     1316 CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG 1375
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Db      440 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu 459

Qy     1376 GGCACCCAGACCTACATCTGCAACGTGAAT 1405
            ||||||||||||||||||||||||||||||
Db      460 GlyThrGlnThrTyrIleCysAsnValAsn 469
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds
                                           (without alignments)
                                           10217.735 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg..........cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
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     1   1405 100.0   1405 13 ADR16814   Adr16814 Human bre
     2 1014.8 72.2   1522 8 ACC00496   Acc00496 Humanised
     3   1003 71.4   1514 12 ADG64751   Adg64751 Humanised
     4   985.8 70.2   1424 13 ADR16815   Adr16815 Human bre
     5   958.4 68.2   5924 3 AAZ38921   Aaz38921 hCAT1 bin
     6   958.4 68.2   5925 3 AAZ38770   Aaz38770 HCAT1 clo
     7   937.8 66.7   2186 10 ADD26469   Add26469 Phagemid
     8   937.8 66.7   2790 10 ADD26467   Add26467 Phagemid
     9   937.8 66.7   2810 10 ADD26471   Add26471 Phagemid
    10   936.4 66.6   1440 10 ADD26475   Add26475 Phagemid

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11      923    65.7    1539    8   AAD56202        Aad56202 X5 antibo
12     916.6   65.2    1539    8   AAD56203        Aad56203 X5 antibo
13     906.2   64.5    1680   12   ADF83552         Adf83552 Anti-tete
14     901.4   64.2    4691    2   AAQ92546        Aaq92546 pComb3 ex
15     901.4   64.2    6166    2   AAQ92547        Aaq92547 Expressio
16     884.8   63.0   10251   10   ABZ37478         Abz37478 CJRA05 nu
17      856    60.9    1526   12   ADN97514         Adn97514 Artificia
18     851.8   60.6    1551   12   ADN97496         Adn97496 Artificia
19     834.8   59.4    1566   12   ADN97494         Adn97494 Artificia
20      834    59.4    2154   12   ADN97490         Adn97490 Artificia
21     820.8   58.4    1572   12   ADN97492         Adn97492 Artificia
22      820    58.4    2160   12   ADN97488         Adn97488 Artificia
23     796.8   56.7    5679   13   ADP79576         Adp79576 Plasmid p
24     779.8   55.5    6563    2   AAV44953        Aav44953 Anti-IL-8
25     779.8   55.5    6563    2   AAX90579        Aax90579 p6G4V11N3
26     779.8   55.5    6563    3   AAZ87970        Aaz87970 Nucleotid
27     779.8   55.5    6563    3   AAC65509        Aac65509 Anti-IL-8
28     779.8   55.5    6563    8   ABX63890        Abx63890 Expressio
29     779.8   55.5    6563    8   ABX81417        Abx81417 Vector p6
30     779.8   55.5    6563   10   AAD59311         Aad59311 p6G4V11 N
31     767.8   54.6    6400    3   AAA53389        Aaa53389 Expressio
32     751.8   53.5    2000    9   ACC70052        Acc70052 Nucleotid
33     747.4   53.2    2178    2   AAQ25592        Aaq25592 Encodes 4
34     747.4   53.2    2178    2   AAV81689        Aav81689 4D5 Fab m
35     739.6   52.6    6072    2   AAV63493        Aav63493 Fab-displ
36     739.6   52.6    6072    6   ABN85200        Abn85200 Phage-dis
37     738.6   52.6    2143    2   AAX03840        Aax03840 Plasmid p
38     738.6   52.6    2143    5   AAF31463        Aaf31463 pS 1130 e
39     737.4   52.5    2050   13   ADR47463         Adr47463 pTTOD(gH3
40     735.2   52.3    6072    2   AAV71266        Aav71266 VEGF huma
41     734.6   52.3    6127    2   AAX07474        Aax07474 Mus muscu
42     734.6   52.3    6127    4   AAF69253        Aaf69253 Expressio
43     734.6   52.3    6127   12   ADN07022         Adn07022 F(ab)-pha
44     733.2   52.2    1951    6   ABQ73919        Abq73919 Plasmid p
45     732.8   52.2    1477   12   ADQ07674         Adq07674 Nucleotid
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RESULT 2
ACC00496
ID   ACC00496 standard; DNA; 1522 BP.
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AC   ACC00496;
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DT   10-JUL-2003   (first entry)
XX
DE   Humanised F3 Fab insert coding sequence.
XX
KW   Cytostatic; Platelet-Derived Growth Factor; PDGF; antibody; tumour;
KW   cancer; F3 antibody; gene; ds.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
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FT   /transl_except= (pos:239. .241,aa:Xaa)

Page 2